Claims-

Please cancel claim 24 without prejudice or disclaimer.

Please add new claims 106-134 as follows:

--106 (new). The monomer polypeptide construct of claim 1, wherein the at least one heterologous moiety is a heterologous moiety which does not exclusively facilitate expression and/or purification of the monomer polypeptide construct.--

--107 (new). The method according to claim 90, wherein the trimeric polypeptide complex is subjected to further processing.--

--108 (new). The trimeric polypeptide complex according to claim 84, wherein the ligand binding structure is selected from the group consisting of a receptor molecule, the ligand binding part of receptor molecule, an antibody, an antigen binding antibody fragment, a molecule having antibody characteristics, a monovalent scFv antibody fragment, and a Fab antibody fragment.--

--109 (new). The trimeric polypeptide complex according to claim 84, wherein the toxin is ricin.--

--110 (new). The trimeric polypeptide complex according to claim 84, wherein the detectable label is selected from the group consisting of a fluorescence labeled molecule, a radioactively labeled molecule, and an enzymatically labeled molecule.--

--111 (new). The trimeric polypeptide complex according to claim 84 wherein the non-proteinaceous polymer is selected from the group consisting of a polymeric alkaloid, a polyalcohol, a polysaccharide, a lipid, and a polyamine.--

--112 (new). An oligomer comprising three monomer polypeptide constructs according to claim 1.--

--113 (new). A monomer polypeptide construct according to claim 1, wherein said TTSE is a polypeptide having at least 68% amino acid sequence identity with the consensus sequence shown in Fig. 2--

--114 (new). A monomer polypeptide construct according to claim 113, wherein the sequence identity with the consensus sequence is at least 81%.--

--115 (new). A monomer polypeptide construct according to claim 114, wherein the sequence identity with the consensus sequence is at least 87%.--

--116 (new). A monomer polypeptide construct according to claim 115, wherein the sequence identity with the consensus sequence is at least 92%.--

--117 (new). A monomer polypeptide construct according to claim 116, wherein the TTSE comprises the consensus sequence shown in Figure 2.--

--118 (new). A monomer polypeptide construct according to claim 1, wherein the TTSE is derived from human tetranectin, murine tetranectin, C-type lectin of bovine cartilage, or C-type lectin of shark cartilage.--

--119 (new). A monomer polypeptide construct according to claim 118, wherein the TTSE is derived from human tetranectin and comprises the amino acid residues V17 to V49 (exon 2) shown in Figure 1.--

--120 (new). A monomer polypeptide construct according to claim 119, wherein the TTSE derived from human tetranectin further comprises the amino acid residues C50 to K52 of exon 3 as shown in Figure 1.--

--121 (new). A monomer polypeptide construct according to claim 1, wherein the monomer polypeptide further comprises the amino acid residues E1 to D16 (exon 1) shown in Figure 1.

--122 (new). A monomer polypeptide construct according to claim 119, wherein at least one amino acid residue of exon 2 selected from the group consisting of amino acid residue nos. 21, 22, 24, 25, 27, 28, 31, 32, 35, 39, 41, 42, is/are substituted by any non-helix breaking amino acid residue, the amino acid residue numbering referring to amino acid residues in SEQ ID NO:7.

--123 (new). A monomer polypeptide construct according to claim 121, wherein amino acid residue no. 6 of exon 1 is substituted by any non-helix breaking amino acid residue, the amino acid residue numbering referring to amino acid residues in SEQ ID NO: 7.

--124 (new). A monomer polypeptide construct according to claim 1, wherein the TTSE comprises a repeated heptad having the formula a-b-c-d-e-f-g (N to C), wherein a majority of the amino acids residues a and d are hydrophobic amino acids.

--125 (new). A monomer polypeptide construct according to claim 124, wherein the heptad is repeated 3 times and wherein the amino acid residues located at sequence positions a and d of the third occurrence of the heptad repeat are glutamine residues.

--126 (new). A monomer polypeptide construct according to claim 1, wherein the at least one heterologous moiety is selected from the group consisting of:

(a) a ligand binding structure;

(b) a toxin;

(c) a detectable moiety;

(d) an in situ activatable substance;

(e) an enzyme;

(f) a radioactive moiety;

(g) a cytokine;

(h) a non-proteinaceous polymer;

(i) a photo cross-linking agent; and

(j) a group facilitating conjugation of the polypeptide to a target, wherein the conjugation encompasses both covalent and non-covalent linkages.--

--127 (new). A monomer polypeptide construct according to claim 126, wherein the ligand binding structure is selected from the group consisting of a receptor molecule,
the ligand binding part of receptor molecule, an antibody, an antigen binding antibody fragment, a molecule having antibody characteristics, a monovalent scFv antibody fragment, and a Fab antibody fragment.--

--128 (new). A monomer polypeptide construct according to claim 126, wherein the toxin is ricin.--

--129 (new). A monomer polypeptide construct according to claim 126, wherein the detectable label is selected from the group consisting of a fluorescence labeled molecule, a radioactively labeled molecule, and an enzymatically labeled molecule.--

--130 (new). A monomer polypeptide construct according to claim 126, wherein the non-proteinaceous polymer is selected from the group consisting of a polymeric alkaloid, a polyalcohol, a polysaccharide, a lipid, and a polyamine.--

--131 (new). A monomer polypeptide construct according to claim 126, wherein said at least one heterologous moiety is positioned C-terminally to the monomer polypeptide.--

--132 (new). A monomer polypeptide construct according to claim 126, wherein said at least one heterologous moiety is positioned N-terminally to the monomer polypeptide.--

--133 (new). A monomer polypeptide construct according to claim 126, which comprises at least one heterologous moiety which is positioned N-terminally to the monomer polypeptide and at least one heterologous moiety which is positioned C-terminally to the monomer polypeptide.--

--134 (new). A monomer polypeptide construct according to claim 126, wherein the at least one heterologous moiety is covalently linked to the monomer polypeptide via a peptide bond to the N- or C-terminus of the monomer polypeptide chain, via a peptide bond to a side chain in the monomer polypeptide, via a bond to a cysteine residue, or when more than one heterologous moiety, combinations of these locations.

Please amend the claims as follows. A version with markings to show changes made to the claims is included herewith as Appendix B.

Please amend claim 1 to recite the following:

--1 (twice amended). A monomer polypeptide construct comprising at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, said TTSE being capable of forming a stable triple alpha helical coiled coil complex

with two other TTSEs, where the heterologous moiety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FCTN23, the sequences of which are shown in SEQ ID NOs:24-27.--

D9

Please amend claim 22 to recite the following:

--22 (twice amended). A trimeric polypeptide complex according to claim 68, wherein the at least one heterologous moiety positioned N-terminally to a TTSE and the at least one heterologous moiety positioned C-terminally to a TTSE are part of the same monomer polypeptide.--

D10

Please amend claim 23 to recite the following:

--23 (twice amended). A trimeric polypeptide complex according to claim 68, wherein the at least one heterologous moiety positioned N-terminally to a TTSE and the at least one heterologous moiety positioned C-terminally to a TTSE are part of two separate monomer polypeptides.--

Please amend claim 68 to recite the following:

--68 (amended). A trimeric polypeptide complex comprising three monomer polypeptides, wherein (i) each of said monomer polypeptides comprises a tetranectin trimerising structural element (TTSE), said TTSE being a polypeptide having at least 68% amino acid sequence identity with the consensus sequence shown in Fig. 2, and (ii) at least one of said monomer polypeptides is covalently linked to at least one heterologous moiety, where said at least one heterologous moiety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FCTN23, the sequences of which are shown in SEQ ID NOs:24-27.--

D11

Please amend claim 76 to recite the following:

--76 (amended). The trimeric polypeptide complex according to claim 75, wherein the TTSE derived from human tetranectin further comprises the amino acid residues C50 to K52 of exon 3 as shown in Figure 1.--

D12

Please amend claim 82 to recite the following:

--82 (amended). The trimeric polypeptide complex according to claim 68 wherein the complex remains substantially as a trimer in the temperature range 50-70°C.--

D13

Please amend claim 84 to recite the following:

--84 (amended). The trimeric polypeptide complex according to claim 68, wherein the at least one heterologous moiety is selected from the group consisting of:

(a) a ligand binding structure;

(b) a toxin;

(c) a detectable moiety;

(d) an in situ activatable substance;

(e) an enzyme;

(f) a radioactive moiety;

D14

(g) a cytokine;

(h) a non-proteinaceous polymer;

(i) a polyalcohol;

(j) a polysaccharide;

(k) a lipid;

(l) a polyamine;

(m) a photo cross-linking agent; and

(n) a group facilitating conjugation of the polypeptide to a target, wherein the conjugation encompasses both covalent and non-covalent linkages.--

Please amend claim 87 to recite the following:

--87 (amended). The trimeric polypeptide complex according to claim 68, which comprises at least one heterologous moiety which is positioned N-terminally to at least one monomer polypeptide and at least one heterologous moiety which is positioned C-terminally to at least one monomer polypeptide.--

D15

Please amend claim 88 to recite the following:

--88 (amended). The trimeric polypeptide complex according to claim 68, wherein the at least one heterologous moiety is covalently linked to the monomer polypeptide via a peptide bond to the N- or C-terminus of the monomer polypeptide chain, via a peptide bond to a side chain in the monomer polypeptide, via a bond to a cysteine residue, or when more than one heterologous moiety, combinations of these locations.--

Please amend claim 90 to recite the following: